

A1
Cont

triads (underlined in Figure 5(a) - SEQ ID NO: 2). The second polypeptide encoded within the *S. pyogenes* database contained several errors that were corrected by our sequencing of this region of the genome. The DNA fragment obtained encoded a protein of 792 amino acids (MW = 87,457 Da) that was 12.6% identical to the pneumococcal sequence and 12.5% identical to the first *S. pyogenes* polypeptide. This predicted amino acid sequence contained four histidine triad motifs (underlined in Fig. 5(b) – SEQ ID NO.: 4). The third polypeptide sequence obtained was one already in the database (Accession No. AF062533) and identified only as an unknown gene downstream from a gene identified as *lmb* in *S. galactiae*. This 822 amino acid protein thus has a predicted molecular weight of 92,353 Da and maintains the 5 histidine triad motifs (underlined in Figure 5(C) - SEQ ID NO: 6). This second polypeptide shows 25.6% sequence identity to Sp36 of pneumococcus type 4 and 97.7% and 11.6% identity to the two group A homologs, respectively.

In the Claims:

✓✓
Please cancel claims 1-8 without prejudice. Please add the following new claims:

*Su
C3*
25. (New) An isolated polypeptide comprising a polypeptide whose amino acid sequence is at least 75% identical to the sequence of SEQ ID NO: 4 and wherein said percent identity differs only by conservative amino acid substitutions.

A2
26. (New) The isolated polypeptide of claim 25 wherein said polypeptide is at least 90% identical to the sequence of SEQ ID NO: 4.

27. (New) The isolated polypeptide of claim 25 wherein said polypeptide is at least 95% identical to the sequence of SEQ ID NO: 4.

28. (New) An isolated polypeptide comprising a polypeptide whose amino acid sequence is at least 75% identical to a sequence selected from the group consisting of